Protein Function Prediction using Multi-label Ensemble Classification

supplementary file

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This is a supplementary file of "Protein Function Prediction using Multi-label Ensemble Classification", which will be published by *IEEE Transactions on Computational Biology and Bioinformatics*.

1 Evaluation Metrics

This section appends the introduction of evaluation metrics (Section 4.2).

Ranking loss evaluates the average fraction of function label pairs that are not correctly ordered:

$$RankingLoss = \frac{1}{u}\sum_{i=l+1}^{N}\frac{1}{|\mathcal{Y}_i||\bar{\mathcal{Y}}_i|}|\{(c_1,c_2)\in \mathcal{Y}_i\times\bar{\mathcal{Y}}_i|F(i,c_1)\leq F(i,c_2)\}|$$

where $\mathcal{Y}_i$ is the function set of protein i, and $\bar{\mathcal{Y}}_i$ is the complement set of $\mathcal{Y}_i$. The performance is perfect when *RankingLoss=0*, and the smaller the value, the better the performance.

Coverage evaluates how far, on average, we need to go down the label ranking list to cover all the ground-truth labels of the instance:

$$Coverage = \frac{1}{u}\sum_{i=l+1}^{N}\max_{c\in\mathcal{Y}_i} rank(F(i,c)) - 1$$

Coverage is often bigger than 1, and the lower the value, the better the performance.

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2 Influence of Different Weighting Schemes

This section appends the results of ***Coverage*** *(in Table 1) with respect to different weighting scheme (Section 5.3).*

3 Influence of Different Ensemble Techniques

This section appends the introduction on different ensemble techniques and the experimental results (Table 2) with respect to Coverage *(Section 5.4).*

Decision templates uses the similarity between the matrix of classifier outputs for an input $\mathbf{x}$ (the Decision Profile $DP(\mathbf{x})$) and the C matrix templates found as the class means of the classifier outputs to determine the likelihood of $\mathbf{x}$ with respect to a specific class [1], [2]. $DP(\mathbf{x})$ for a sample $\mathbf{x}$ is a matrix composed of the entries $d_{r,c}(\mathbf{x})\in[0,1]$ $(r=1,...,R; c=1,...,C)$, each entry represents the support given by the r-th classifier to class c. Decision templates DT_c are the averaged decision profiles obtained from $\mathbf{X}_c$, which includes the set of training samples belonging to the c-th class.

$$DT_c = \frac{\sum_{\mathbf{x}\in\mathbf{X}_c} DP(\mathbf{x})}{|\mathbf{X}_c|}$$

For a test sample $\mathbf{x}$, its similarity between decision profile $DP(\mathbf{x})$ and the c-th decision template DT_c is computed as:

$$sim(\mathbf{x},c) = 1 - \frac{1}{R\times C}\sum_{r=1}^{R}\sum_{m=1}^{C}(DT_c(r,m) - d_{r,m}(\mathbf{x}))^2$$

$sim(\mathbf{x},c)$ can be viewed as the predicted likelihood of $\mathbf{x}$ with respect to the c-th class.

The linear regression based ensemble combines R classifiers by optimizing a linear regression problem as follows [3]:

$$\begin{aligned}\arg\min_{\boldsymbol{\omega}_c}\sum_{r=1}^{R}\sum_{i=1}^{l}(\omega_{rc}F_r(\mathbf{x}_i,c)-\mathbf{y}_{ic})^2+\mu\|\boldsymbol{\omega}_c\|^2 \\ = \arg\min_{\boldsymbol{\omega}_c}\|\mathbf{F}_{lc}\boldsymbol{\omega}_c-\mathbf{Y}_{lc}\|^2+\mu\|\boldsymbol{\omega}_c\|^2\end{aligned}$$

TABLE 1
Coverage (avg±std) on **Yeast (44 kernels)**, **Human (8 kernels)** and **Fly (38 kernels)**, with respect to different weighting schemes.

	Yeast		Human		Fly	
	20%	50%	20%	50%	20%	50%
TMC-B	25.16±0.67	22.04±0.57	84.74±1.98	65.23±1.69	188.79±3.35	153.30±2.45
TMC-BW	23.25±0.65	20.06±0.51	83.78±1.97	63.99±1.65	178.35±3.23	141.71±2.53
TMC-E	22.61±0.67	18.81±0.44	93.32±2.07	78.73±1.47	173.48±2.86	135.80±2.83
TMEC	**21.30±0.52**	**17.72±0.40**	**79.07±1.60**	**59.67±1.55**	**166.80±2.39**	**132.02±3.19**

where ω_{rc} is the weight of the r-th classifier with respect to the c-th label. $\mathbf{F}_c = [\mathbf{F}_{1c}, \mathbf{F}_{2c}, \cdots, \mathbf{F}_{Rc}] \in \mathbb{R}^{N\times R}$, $\mathbf{F}_{rc} \in \mathbb{R}^N$ is F_r predicted likelihood vector with respect to the c-th label on N samples, and $\mathbf{F}_{lc}$ is the first l rows of $\mathbf{F}_c$. $\mathbf{y}_{ic} = 1$ if the i-th sample has the c-label, and $\mathbf{y}_{ic} = 0$ otherwise. $\mathbf{Y} = [\mathbf{y}_1, ..., \mathbf{y}_N] \in \mathbb{R}^{N\times C}$ is the initial labels on N samples and $\mathbf{Y}_{lc}$ is the first l rows with respect to the c-th column of $\mathbf{Y}$. μ is set to balance the importance of the first term and the second term. Our aim in using ω_{rc} is that different classifiers may have different weights on the c-th label. The analytical solution of $\boldsymbol{\omega}_c$ is:

$$\boldsymbol{\omega}_c = (\mathbf{F}_{lc}^{\mathrm{T}}\mathbf{F}_{lc} + \mu\mathbf{I}_R)^{-1}\mathbf{F}_{lc}^{T}\mathbf{Y}_{lc}$$

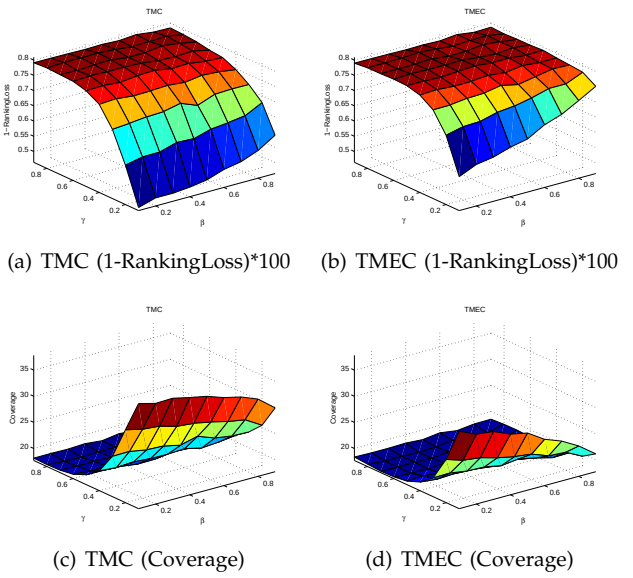
where $\mathbf{I}_R$ is a $R \times R$ identity matrix. Let $\mathbf{W} = [\boldsymbol{\omega}_1^{\mathrm{T}}, \boldsymbol{\omega}_2^{\mathrm{T}}, \cdots, \boldsymbol{\omega}_C^{\mathrm{T}}] \in \mathbb{R}^{R\times C}$, then the ensemble predicted likelihood vector is:

$$f(\mathbf{x}) = \sum_{r=1}^{R} \mathbf{W}_r \circ F_r(\mathbf{x})$$

where $\circ$ is the element-wise multiplication operator.

TABLE 2
Performance (*Coverage*) with respect to different ensemble techniques.

Methods	Yeast	Human	Fly
TMEC	**18.20±0.54**	**62.99±1.55**	**145.45±3.73**
TMEC-DT	27.28±0.25	111.82±0.76	189.87±1.52
TMEC-Reg	30.97±0.73	115.05±3.42	254.71±6.23



(a) TMC (1-RankingLoss)*100 (b) TMEC (1-RankingLoss)*100

(c) TMC (Coverage) (d) TMEC (Coverage)

Fig. 1. *1-RankingLoss* and *Coverage* on different β and γ **(Yeast)**. Similar colors in the figure are parameters with similar predictive performance.

4 Parameter Sensitivity Analysis

*This section appends the results of the parameter sensitivity analysis (Fig. 1) on **Yeast** (Section 5.5).*

References

[1] L. I. Kuncheva, J. C. Bezdek, and R. Duin, "Decision templates for multiple classifier fusion: an experimental comparison," *Pattern Recognition*, vol. 34, no. 2, pp. 299–314, 2001.

[2] M. Re and G. Valentini, "Ensemble based data fusion for gene function prediction," *Multiple Classifier Systems*, pp. 448–457, 2009.

[3] G. Yu, G. Zhang, Z. Zhang, Z. Yu, and L. Deng, "Semi-supervised classification based on subspace sparse representation," *Knowledge and Information Systems, Minor Revision and Resubmitted on 2013-06-29.*